

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model  
Run on: March 9, 2002, 00:09:27 ; Search time 8498.8 Seconds  
(without alignments)  
30.345 Million cell updates/sec

Title: US-09-851-670-16  
Perfect score: 24  
Sequence: 1 gtccaaaggagagaatttctgca 24  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues  
Total number of hits satisfying chosen parameters: 111874  
Minimum DB seq length: 0  
Maximum DB seq length: 60

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database : EST:\*

1: em\_estfun:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_eston:\*

5: em\_esttpi:\*

6: em\_estba:\*

7: em\_estro:\*

8: em\_estov:\*

9: em\_htc:\*

10: gb\_est1:\*

11: gb\_htc:\*

12: gb\_gss:\*

13: gb\_gss\_fun:\*

14: em\_gss\_hum:\*

15: em\_gss\_inv:\*

16: em\_gss\_pln:\*

17: em\_gss\_pro:\*

18: em\_gss\_rnd:\*

19: em\_gss\_vrt:\*

20: em\_gss\_other:\*

21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	15.8	65.8	51 13 A2793014	A2793014 2M0045E17
2	15.2	63.3	59 13 A2Z61084	A2Z61084 1M0104D08
C 3	14.4	60.0	54 13 A2Z21737	A2Z21737 1006031H1
C 4	14	58.3	39 11 BF339449	BF339449 602039103
C 5	14	58.3	39 11 BF342092	BF342092 602012848
C 6	13.8	57.5	29 13 A2Z658555	A2Z658555 1M0535113
C 7	13.8	57.5	39 10 AU011691	AU011691 AU011691
C 8	13.4	55.8	43 13 A2Z69134	A2Z69134 2M0181E10
C 9	13.4	55.8	51 10 AU013478	AU013478 AU01378
C 10	13.2	55.0	29 13 A2Z88457	A2Z88457 1M0396L17
C 11	13.2	55.0	42 13 A2Z32296	A2Z32296 1M0487E12
C 12	13.2	55.0	57 10 AL595919	AL595919 AL595919

8

Result No. Score Query Length DB ID Description

RESULT	1	LOCUS	A2793014	51 bp DNA	GSS	16-FEB-2001
DEFINITION			clone UGGC2h0045E17 R.	DNA sequence.	Mus	musculus genomic
ACCESSION	A2793014					
VERSION	A2793014.1					
KEYWORDS	GSS,					
SOURCE						
ORGANISM	house mouse.					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus.					
REFERENCE	1 (bases 1 to 51)					
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenem,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.					
TITLE	Mouse whole genome scaffolding with paired end reads from 10 kb plasmid inserts					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Robert B. Weiss					
	University of Utah Genome Center					
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT					
	84112, USA					
	tel: 801 585 5606					
	fax: 801 585 7177					
	email: ddunn@genetics.utah.edu					
	Insert length: 10000 Std Error: 0.00					
	Plate: 0045 row: E column: 17					
	Seq primer: CACAGGAAACGCTATGACC					
	Class: Plasmid ends					
	High quality sequence stop: 51.					
	Location/Qualifiers					
	1. .51					

source  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0045E17"  
 /clone\_libr="Mouse 10kb plasmid uggc1m library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.Jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g11473114gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." (Stratagene) cells  
 BASE COUNT 15 a 12 c 13 g 11 t  
 ORIGIN  
 Query Match 65.8%; Score 15.8; DB 13; Length 51;  
 Best Local Similarity 89.5%; Pred. No. 5.9e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 gttccaaaggcaggcaattt 19  
 Db 27 GTCCAAGGGCAGGCAATAT 45  
 RESULT 2  
 AZ361084 AZ361084 59 bp DNA GSS 02-OCT-2000  
 DEFINITION IM0104D08R Mouse 10kb plasmid UGGC1M library Mus musculus genomic clone UGGC1M0104D08 R, DNA sequence.  
 ACCESSION AZ361084  
 VERSION AZ361084.1 GI:1047784  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 59)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvall, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D. Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5506  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0104 row: D column: 08  
 Seq Primer: CACACAGGAAACAGCTTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 59.  
 FEATURES source  
 /organism="Zea mays"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 FEATURES source  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGC1M0104D08"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.Jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g11473114gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." (Stratagene) cells  
 BASE COUNT 15 a 9 c 18 g 17 t  
 ORIGIN  
 Query Match 63.3%; Score 15.2; DB 13; Length 59;  
 Best Local Similarity 85.0%; Pred. No. 1.1e+04;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 5 aaggcagacaatcttcgtca 24  
 Db 19 AAGCCAGAGTCAGTCTGC 38  
 RESULT 3  
 AZ911737/C  
 LOCUS A2921737 54 bp DNA GSS 20-MAR-2001  
 DEFINITION 1006031H12.y1 1006 - Rescuem Grid G zea mays genomic, DNA sequence.  
 ACCESSION A2921737  
 VERSION A2921737.1 GI:13393675  
 KEYWORDS GSS,  
 SOURCE zea mays.  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 54)  
 AUTHORS Walbot, V.  
 TITLE Maize genomic sequences found using engineered Rescuem transposon unpublished (2001)  
 JOURNAL Contact: Walbot, V  
 COMMENT Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Possible ligations site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence.  
 Plate: 1006031 row: H column: 12  
 Class: transposon-tagged  
 Location/Qualifiers 1. .54  
 FEATURES source  
 /organism="Zea mays"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"



**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

**JOURNAL** Unpublished (2000)

**COMMENT** Contact: Robert B. Weiss

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tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0535 row: I column: 13

Seq primer: CGTGTAAACGACGCCAGT

Class: Plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

1. .29

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:0090"

/clone="UUGCIM055113"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.Jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (914732114|gb) (AF29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**BASE COUNT**

ORIGIN

5 a 5 c 8 g 11 t

**FEATURES**

source

**REFERENCE**

1. (bases 1 to 39)

**AUTHORS** Morimyo, M. and Mita, K.

**TITLE** Identification of expressed sequence tags of *Schizosaccharomyces pombe* Unpublished (1998)

**JOURNAL** Contact: Mitsuko Morimyo

National Institute of Radiological Sciences 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan

Email: morimyo@nirs.go.jp

**COMMENT** Location/Qualifiers

1. .39

/organism="Schizosaccharomyces pombe"

/strain="972"

/db\_xref="taxon:496"

/clone="spc1157"

/clone\_id="Schizosaccharomyces pombe late log phase cDNA"

/sex="h minus"

/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp/>)"

**BASE COUNT**

10 a 11 c 5 g 12 t 1 others

**FEATURES**

source

**REFERENCE**

1. (bases 1 to 39)

**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

**TITLE** Unpublished (2000)

**JOURNAL** Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0181 row: E column: 10

Seq primer: CGTGTAAACGACGCCAGT

Class: Plasmid ends

High quality sequence stop: 43.

Location/Qualifiers

1. .43

**FEATURES**

source

/organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGC0M01B1E10"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold,  $\lambda$ -resistant, F-"  
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.Jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor Oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT	ORIGIN
8 a	17 c
17 c	5 g
5 g	13 t

Query Match 55.8%; Score 13.4; DB 10; Length 51;  
 Best Local Similarity 73.9%; Pred. No. 6.5e+04;  
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 10 agagaattttctgca 24  
 Db 41 AGGCAAGTTCTGCA 27

RESULT 10  
 AU013478 LOCUS A2588457 29 bp DNA GSS 13-DEC-2000  
 DEFINITION 1M0396L17R Mouse 10kb plasmid UGGC1M library Mus musculus genomic clone UGGC1M0396L17 R, DNA sequence.  
 ACCESSION A2588457  
 VERSION A2588457.1 GI:11710647  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 REFERENCE 1 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 AUTHORS Dunn,D., Avioli,A., Barber,M., Beacons,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenah,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 COMMENT Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 University of Utah Genome Center  
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: downinggenetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0396 Row: L column: 17  
 Seq primer: CACAGAGAACAGCTATGCC  
 Class: Plasmid ends  
 High quality sequence stop: 29.  
 Location/Qualifiers

FEATURES source  
 1..29  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGGC0M0396L17"  
 /clone.lib="Mouse 10kb Plasmid UGGC1M library"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold,  $\lambda$ -resistant, F-"  
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.Jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor Oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT  
5 a 9 c 5 g 10 t  
ORIGIN

Query Match 55.0%; Score 13.2; DB 13; Length 29;  
Best Local Similarity 83.3%; Pred. No. 7.7e+04;  
Matches 15; Conservative 0; Mismatches 3;  
Indels 0; Gaps 0;  
Qy 6 agccagagaatctcgc 23  
Db 29 AGGRANGGGCAATTTCAGC 12

RESULT 11

AZ332796/c  
LOCUS A2632796 42 bp DNA GSS 13-DEC-2000  
DEFINITION 1M0487E12R Mouse 10kb plasmid UGGC1M library Mus musculus genomic  
ACCESSION clone UGGC1M0487E12 R, DNA sequence.  
VERSION A2632796.1 GI:11754986  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
1 (bases 1 to 42)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beaumont,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
tel: 801 585 5506  
fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0487 row: E column: 12  
Seq primer: CACACAGGAAACAGCTATGAC  
Class: plasmid ends  
High quality sequence stop: 42.

FEATURES source  
1. .42  
/Location/Qualifiers  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0487E12"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/sex="Male"  
/note="Vector: pMD42uv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.Jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD2 (gi|4721149|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated

BASE COUNT  
8 a 5 c 8 g 21 t  
ORIGIN

Query Match 55.0%; Score 13.2; DB 13; Length 42;  
Best Local Similarity 83.3%; Pred. No. 7.8e+04;  
Matches 15; Conservative 0; Mismatches 3;  
Indels 0; Gaps 0;  
Qy 2 tcacaggcagacaattt 19  
Db 28 TCCAAAGGCAGACATT 11

RESULT 12

AL595919/c  
LOCUS AL595919 57 bp mRNA EST 30-JUL-2001  
DEFINITION mRNA sequence.  
ACCESSION AL595919  
VERSION AL595919  
KEYWORDS EST.  
SOURCE Silurana tropicalis  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
Xenopodinae; Silurana.  
1 (bases 1 to 57)  
AUTHORS Huckle,E., Taylor,R., McMurray,A., Ashurst,J.L., Zorn,A.M. and  
Roger,J.  
TITLE Sanger Xenopus tropicalis EST project 2001  
JOURNAL Unpublished (2001)  
COMMENT Contact: Huckle E  
Sanger Centre  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: tropes.sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE\_ID: TGas004019.sp6  
Sequencing primer: SP6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Aaron M. Zorn.  
Location/Qualifiers

FEATURES source  
1. .57  
/Location/Qualifiers  
/organism="Silurana tropicalis"  
/db\_xref="taxon:8364"  
/clone="TGas004019"  
/clone\_id="XGC-gastrula"  
/dev\_stage="gastrula (stages 10-5-13 mixed)"  
/lab\_host="Escherichia coli DH10B"  
/note="Vector: pCS107; Site\_1: EcoRI; Site\_2: NotI; cDNA  
was oligo dT primed from 5ug of poly A+ RNA from stages  
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated  
into pCS107 with EcoRI at the 5' end and NotI at the 3'  
end."  
BASE COUNT  
11 a 28 c 10 g 8 t  
ORIGIN

Query Match 55.0%; Score 13.2; DB 10; Length 57;  
Best Local Similarity 83.3%; Pred. No. 7.9e+04;  
Matches 15; Conservative 0; Mismatches 3;  
Indels 0; Gaps 0;  
Qy 7 ggccagagaatccgtca 24  
Db 56 GGCAAGGCATTCCTCGCA 39

RESULT 13

AU105510

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

LOCUS AU105510 50 bp mRNA EST 05-APR-2001  
DEFINITION AU105510 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
CAS08101, mRNA sequence.

ACCESSION AU105510  
VERSION AU105510.1 GI:13555031  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)  
AUTHORS Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo ,K., Sugano,A. and Sugano,S.

TITLE Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries  
JOURNAL Unpublished (2001)  
COMMENT Contact: Yutaka Suzuki  
Department of Virology, University of Tokyo  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Sugano,A. and Sugano ,S. Construction and characterization of a full length-enriched and a 5'-end enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES source  
ORIGIN

BASE COUNT 7 a 14 c 18 g 11 t  
ORIGIN

Query Match 54.2%; Score 13; DB 10; Length 50;  
Best Local Similarity 76.2%; Pred. No. 9.6e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
/clone-lib="Sugano Homo sapiens cDNA library"  
/db-xref="CA08101"

Query Match 54.2%; Score 13; DB 10; Length 50;  
Best Local Similarity 76.2%; Pred. No. 9.6e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
/clone-lib="Sugano Homo sapiens cDNA library"  
/db-xref="CA08101"

RESULT 15  
LOCUS AU105525 50 bp mRNA EST 05-APR-2001  
DEFINITION AU105525 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
HRC03805, mRNA sequence.

ACCESSION AU105525  
VERSION AU105525.1 GI:13555046  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)  
AUTHORS Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo ,K., Sugano,A. and Sugano,S.

TITLE Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries  
JOURNAL Unpublished (2001)  
COMMENT Contact: Yutaka Suzuki  
Department of Virology, University of Tokyo  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Sugano,A. and Sugano ,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES source  
ORIGIN

BASE COUNT 6 a 15 c 15 g 14 t  
ORIGIN

Query Match 54.2%; Score 13; DB 10; Length 50;  
Best Local Similarity 76.2%; Pred. No. 9.6e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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FEATURES source  
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Job time: 11044 sec

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Mon Mar 11 07:46:32 2002

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